SEQUENCE LISTING

<110> BATHE, Brigitte

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ppsA GENE

<130> DE/SD1 WP 215

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<170> PatentIn version 3.1

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cgcttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcacgcaac     180

tcattaaacg attgttgttc cataagacca tcatcgttgt ttttttagaa aattgc ctg     239
                                                                          Met
                                                                          1

cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga       287
Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
            5                   10                  15

ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac       335
Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
            20                  25                  30

ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct       383
Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
        35                  40                  45

aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att       431
Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
50                  55                  60                  65

tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcg gtc       479
Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
                70                  75                  80

gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg       527
Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
            85                  90                  95

atc ggc acc gat gtg cac gaa att ttt gac cgc cac cta aat ggc cga       575
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Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
        100                 105                 110


gaa atc acc gtt ctc aat gac gca gat gcc gcc ggc atc gcc gaa gca    623
Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu Ala
        115                 120                 125


acc ttt ggc aac cct gcc gca cgc gaa ggc gca gtc atc ctg ctg acc    671
Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu Thr
130                 135                 140                 145


ctt ggt aca ggt att gga tcc gca ttc ctt gtg gat ggc caa ctg ttc    719
Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu Phe
                    150                 155                 160


ccc aac aca gaa ctt ggt cac atg atc gtt gac ggc gag gaa gca gaa    767
Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala Glu
                165                 170                 175


cac ctt gca gca gca tcc gtc aaa gaa aac gaa gat ctg tca tgg aag    815
His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp Lys
            180                 185                 190


aaa tgg gcg aag cac ctg aac aag gtg ctg agc gaa tac gag aaa ctt    863
Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys Leu
        195                 200                 205


ttc tcc cca tcc gtc ttc atc atc ggt ggc gga att tcc aga aag cac    911
Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys His
210                 215                 220                 225


gaa aag tgg ctt cca ttg atg gag cta gac act gac att gtc cca gct    959
Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro Ala
                    230                 235                 240


gag ctg cgc aat cga gcc gga atc gta gga gct gcc atg gca gta aac    1007
Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val Asn
                245                 250                 255


caa cac ctc acc cca taagttatcg aaaggtgatt tttgcccagg gccttgattc    1062
Gln His Leu Thr Pro
                260


acaacgcacc ttgctgtagg aaaaacaggc ccctttgtga catcggcgta gttgttcaac    1122


tataatggaa cgctgatcgt ggacaagagt taaccatgag attgattcac ccctttaagc    1132


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Met Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr
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Gly His Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val
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Asn Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr
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Pro Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile
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Ile Ser Gln Ala Gln Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser
65   70   75   80

Val Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser
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Trp Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly
                100   105   110

Arg Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu
        115   120   125

Ala Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu
        130   135   140

Thr Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu
145   150   155   160

Phe Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala
                165   170   175

Glu His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp
                180   185   190

Lys Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys
                195   200   205

Leu Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys
        210   215   220

His Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro
225   230   235   240

Ala Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val

Page 3

245   250   255

Asn Gln His Leu Thr Pro
        260